



atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc gga cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro	
65 70 75 80	
gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala	
100 105 110	
aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act	528
Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr	
165 170 175	
aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	

FIG. 1A



cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt	768
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val	
245 250 255	
gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt	816
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly	
260 265 270	
tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr	
275 280 285	
ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly	
290 295 300	
tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac	960
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

FIG. 1B



atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc ggt cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca	240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro	
65 70 75 80	
gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca	288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa	336
Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu	
100 105 110	
aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cac gca tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gca ggt gct gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	

FIG. 2A



cct	aac	tca	act	ggg	gct	gca	aaa	gct	atc	gga	ctt	gtt	atc	cca	gaa	672
Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu	
	210						215				220					
ttg	aac	ggg	aaa	ctt	gat	ggg	gct	gca	caa	cgt	gtt	cct	gtt	cca	act	720
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr	
225					230					235					240	
gga	tca	gta	act	gaa	ttg	gtt	gca	act	ctt	gaa	aaa	gac	gta	act	gtc	768
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Thr	Leu	Glu	Lys	Asp	Val	Thr	Val	
				245					250					255		
gaa	gaa	gta	aat	gca	gct	atg	aaa	gca	gca	gct	aac	gat	tca	tac	ggg	816
Glu	Glu	Val	Asn	Ala	Ala	Met	Lys	Ala	Ala	Ala	Asn	Asp	Ser	Tyr	Gly	
			260					265					270			
tat	act	gaa	gat	cca	atc	gta	tca	tct	gat	atc	gtt	ggg	att	tca	tac	864
Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Ile	Ser	Tyr	
		275					280					285				
ggg	tca	ttg	ttt	gat	gct	act	caa	act	aaa	gtt	caa	act	gtt	gac	ggg	912
Gly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Gln	Thr	Val	Asp	Gly	
	290					295					300					
aac	caa	ttg	gtt	aaa	gtt	gtt	tca	tgg	tac	gat	aac	gaa	atg	tca	tac	960
Asn	Gln	Leu	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Met	Ser	Tyr	
305					310					315					320	
act	tca	caa	ctt	gtt	cgt	aca	ctt	gag	tac	ttt	gca	aaa	atc	gct	aaa	1008
Thr	Ser	Gln	Leu	Val	Arg	Thr	Leu	Glu	Tyr	Phe	Ala	Lys	Ile	Ala	Lys	
				325				330						335		
taa																1011

FIG. 2B



atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc gga cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgt att caa aac gtt gaa ggt gtt gaa gta act cgt att	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gat ctt act gac cca aat atg ctt gca cac ttg ttg aaa tat gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttc gac ggt aca gtt gaa gtt aaa gat ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
50 55 60	
ttc gaa gtt aac gga aac ttc atc aaa gtt tct gct gaa aaa gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro	
65 70 75 80	
gaa aac att gac tgg gca act gac ggt gta gaa atc gtt ctt gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Glu Lys His Leu His Ala	
100 105 110	
aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga gat gat gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val	
115 120 125	
aaa act gtt gta ttt aac aca aac cat gac att ctt gac ggt aca gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
act gta att tca ggt gct tca tgt act act aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cac gct tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gca agc aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val	
195 200 205	

FIG. 3A



09878781.091002

cct aac tca act ggt gct gct aaa gca atc ggt ctt gta atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gaa act tca gtt	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val	
245 250 255	
gaa gaa atc aac gca gca atg aaa gca gct gca aac gat tca tac gga	816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gac cca atc gta tct tct gat atc atc ggt atg gct tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr	
275 280 285	
ggt tca ttg ttt gat gct act caa act aaa gta caa act gtt gat gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aat caa tta gtt aaa gtt gtt tca tgg tat gac aac gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gca caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

FIG. 3B



atg gta gtt aaa gtt ggt att aac ggt ttt ggc cgt atc gga cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gct ttc cgt cgt att caa aat gta gaa ggt gtt gaa gtt act cgc atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aat atg ctt gca cac ttg tta aaa tac gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttt gac ggt act gta gaa gtt aaa gat ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
50 55 60	
ttt gac gtt aac gga aaa ttc att aaa gtt tct gct gaa aaa gat cca	240
Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro	
65 70 75 80	
gaa caa att gac tgg gca act gac ggt gtt gaa atc gtt ctt gaa gca	288
Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gaa	336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Glu Lys His Leu His Glu	
100 105 110	
aat ggt gct aaa aaa gtt gtt atc act gct cct ggt gga gat gac gtg	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val	
115 120 125	
aaa aca gtt gta ttt aac act aac cat gat atc ctt gat gga act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt att tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct tta caa gat aac ttt ggc gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
aca atc cac gct tac act ggt gat caa atg ctt ctt gat gga cct cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val	
195 200 205	

FIG. 4A



09878781.091002

cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cct gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
tta aat ggt aaa ctt gac ggt gct gca caa cgt gta cca gtt cca aca	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
ggt tca gta aca gaa tta gta gca gtt ctt aat aaa gaa act tca gta	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val	
245 250 255	
gaa gaa att aac tca gta atg aaa gct gca gct aat gat tca tat ggt	816
Glu Glu Ile Asn Ser Val Met Lys Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gat cca atc gta tca tct gat atc gtt ggt atg tct ttc	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe	
275 280 285	
ggt tca tta ttc gat gct act caa act aaa gta caa act gtt gat gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aat caa tta gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gct caa ctt gat cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

FIG. 4B





09878781.091002

atg gta gtt aaa gtt ggt att aac ggt ttc gga cgt atc ggt cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
50 55 60	
ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca	240
Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro	
65 70 75 80	
gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca	288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala	
85 90 95	
aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct	336
Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala	
100 105 110	
aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt tac aac act aac cat gat att ctt gat gga act gaa	432
Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cat ggt tac act ggt gac caa atg gtt ctt gac gga cca cac	576
Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gat ctt cgt cgt gct cgt gca gct gca gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val	
195 200 205	

FIG. 5A



cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu 210 215 220	672
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr 225 230 235 240	720
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val 245 250 255	768
gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly 260 265 270	816
tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr 275 280 285	864
ggt tca tta ttt gat gct act caa act aaa gta caa act gtt gat gga Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly 290 295 300	912
aat caa ttg gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr 305 310 315 320	960
act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys 325 330 335	1008
taa	1011

FIG. 5B



	1				50
DysGapC	ATGGTAGTTA	AAGTTGGTAT	TAACGGTTTC	GGTCGTATCG	GACGTCTTGC
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
ParaUbGapC	-----	-----	-----t	--c-----	-----
UberGapc	-----	-----	-----	-----	-----
AgalGapCDNA	-----	-----	-----	-----	-t-----
SiniGapC	-----	-----	-----	--a-----	-t-----
BovGapC	-----	-----	-----	---c---	-g-c-g-t
	51				100
DysGapC	ATTCCGTCGT	ATTCAAAATG	TTGAAGGTGT	TGAAGTAACT	CGTATCAACG
SpyGapC	-----c---	-----ca	-c-----	-----	-----t-
SeqGapC	-----	-----	-----	-----	-----
ParaUbGapC	t-----	-----	-a-----	-----t--	--c-----
UberGapc	-----	-----c-	-----	-----	-----t--
AgalGapCDNA	-----c	--c-----c-	-a-----	-----t--	-----
SiniGapC	-----	-----	-----	-----	-----t-
BovGapC	cac-a-ggc-	gc-ttt---t	c--gcaaa--	g--ca-cgtc	gcc-----t-
	101				150
DysGapC	ACC...TTAC	AGATCCAAAC	ATGCTTGCAC	ACTTGTTGAA	ATACGATACA
SpyGapC	---...-----	-----t	-----	-----	---c-----
SeqGapC	---...-----	-----	-----	-----	---c-----
ParaUbGapC	---...-----	-----t	-----	-----a--	---c-----
UberGapc	-t-...-----	t--c-----t	-----	-----	---t-----
AgalGapCDNA	---...-----	-----	-----	-----	---t-c---
SiniGapC	---...-----	-----t--	-----	-----	---t-----
BovGapC	---cct-c-t	t--c-ttc--	taca-g-tct	--a---cc-	g--t---t-c

FIG. 6A



09878781.091002

	151				200
DysGapC	ACTCAAGGAC	GTTTTGACGG	AACTGTTGAA	GTTAAAGAAG	GTGGATTGTA
SpyGapC	-----	-----t--	a--a-----	-----	-----t--
SeqGapC	-----a-	-----	a--t-----	-----	-----t--
ParaUbGapC	-----	-----	--t--a---	-----t-	-----t--
UberGapC	-----	-----c---	--a-----	-----t-	-----c--
AgalGapCDNA	-----	-----c---	--t-----	-----	-----c--
SiniGapC	-----	-----	--a-----	-----t-	-----c--
BovGapC	--c--c--ca	ag--ca---	c--a--ca-g	-cag-ga-c-	-gaagc-c-t
	201				250
DysGapC	AGTAAACGGA	AACTTCATCA	AAGTTTCTGC	TGAACGTGAT	CCAGAAAACA
SpyGapC	---a-----	-----	-----	-----t--	-----
SeqGapC	---a-----	-----	-----	-----t--	-----
ParaUbGapC	c-----	--a----t-	-----	---aaa---	-----c-a-
UberGapC	-----	-----	-----	---aaa---	-----
AgalGapCDNA	-----t	c-a--tg-t-	-----	-----c-a	-----c----
SiniGapC	-----	-g--tg-t-	-----	a-----c-a	-----c----
BovGapC	ca-c--t---	--ggc----	cca-c-tcca	g--g--a---	--t-cc----
	251				300
DysGapC	TCGACTGGGC	AACTGACGGT	GTTGAAATCG	TTCTGGAAGC	AACTGGTTTC
SpyGapC	-c-----	-----t--g	-----	-----	-----
SeqGapC	-c-----	-----c--	-----	-----	-----
ParaUbGapC	-t-----	-----c--	-----	-----	-----
UberGapC	-t-----	-----c--	--a-----	-----	-----
AgalGapCDNA	-t-----	t----t--c	--a-----	-----	-----
SiniGapC	-t-----	t----t--	--a--c---	-----	-----a-----
BovGapC	-ca-g---g	tga--ct---	-c---gtat-	-ag-g--gt-	c----gg--
	301				350
DysGapC	TTTGCTAAAA	AAGAAGCTGC	TGAAAAACAC	TTACATGCTA	ACGGTGCTAA
SpyGapC	-----	-----a-	-----	-----	-----
SeqGapC	-----	-----	-----c-	-----	-----
ParaUbGapC	-----	-----c-----	-----t	-----aa-	-t-----
UberGapC	-----	-----c-----	-----t	-----	-----
AgalGapCDNA	-----atc--	-----aaa-	--g-c-----	a-c---aa-	-t-----
SiniGapC	--c---tct-	-----c-----	-----c-----	a-t--c-----	-----g--
BovGapC	--ca---cc-	tg--gaag--	--gggct---	--ga-g-g-	...-c--c--
	351				400
DysGapC	AAAAGTTGTT	ATCACAGCTC	CTGGTGGAAG	CGACGTTAAA	ACAGTTGTTT
SpyGapC	-----	-----	-----	-----t	-----
SeqGapC	-----	-----	-----	-----	-----
ParaUbGapC	-----	-----t---	-----g-	t-----g--	-----a-
UberGapC	-----	-----	-----g-	t--t-----	--t-----a-
AgalGapCDNA	-----	-----	-----	-----	-----
SiniGapC	-----	-----	-----	t-----	-----
BovGapC	g-gg--ca-c	---t-t--a-	--tc---...c	---t-cccc	-tgt---ga

FIG. 6B



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	401				450
DysGapC	TCAACACTAA	CCACGA.CAT	TCTTGACGGT	ACTGAAACAG	TTATCTCAGG
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
ParaUbGapC	-t-----	---t-.t--	c-----t-a	-----	---t-----
UberGapC	-t-----a--	---t-.---	-----	--a-----t-	-a-t-----
AgalGapCDNA	-----	-----t-	c-----t-a	-----	-----
SiniGapC	a-----	---t-.t--	-----t-a	-----	-----
BovGapC	-ggg-gtg--	-----a-g	-.a-a-aac	--cctc-aga	--g--agcaa
	451				500
DysGapC	TGCTTCATGT	ACTACAAACT	GTTTAGCTCC	TATGGCTAAA	GCTCTTCACG
SpyGapC	-----	-----	-----	t-----	---c-t--c-
SeqGapC	-----	-----	-----	t-----	---c-t--c-
ParaUbGapC	-----	-----	-----	-----	---a-----
UberGapC	-----	-----t-	-----	-----	---g-----
AgalGapCDNA	-----	-----	---c-t---	-----	---a-----
SiniGapC	-----	-----	-----	-----	---a-a-----
BovGapC	---c--c--c	--c--c---	-c-g--c--	cc---c--g	-tca-c--t-
	501				550
DysGapC	ATGCATTGG	TATCCAAAAA	GGTCTTATGA	CTACAATCCA	CGCTTATACT
SpyGapC	--gca--c--	-a--c--a--	---c-----	---a-----	-----
SeqGapC	--gca-----	-a--c--a--	---c-----	---a-----	-----
ParaUbGapC	-----	cg-a-----	---t-a---	---a-----	-----
UberGapC	-----	-g-----	---t-g---	-a-t-----	-----
AgalGapCDNA	-c-----	-g-----	---t-g---	---t-----	---a-----
SiniGapC	-----	-g-a-----	---t-a---	---t-----	t-g-----
BovGapC	-cc-----	ca-cgtgg-g	--ac-----	-c-tg---	---cat---
	551				600
DysGapC	GGTGACCAAA	TGATCCTTGA	CGGACCACAC	CGTGGTGGTG	ACCTTCGTCG
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	---g---	t---ac-gt	g-----	-t-----
ParaUbGapC	---t---	--c-t---	t---t---	-----	---t-a---
UberGapC	-----	-----	-----	-----	-----
AgalGapCDNA	-----	-----	-----	-----	-----
SiniGapC	-----	--g-t---	-----	-----	-t-----
BovGapC	-ccac---g	a--ctg-g--	t--c--ctc-	...--gaagc	tgtgg---ga
	601				650
DysGapC	TGCTCGTGCT	GGTGCTGCAA	ACATTGTTCC	TAACTCAACT	GGTGCTGCTA
SpyGapC	---a--c---	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----cg--
ParaUbGapC	---c-----	-----aac-	-t--t---	-----	-----
UberGapC	-----	-----aagc-	---t---	-----	-----
AgalGapCDNA	-----a	-----	-----	-----	-----a-
SiniGapC	-----a	-c--a---	-----	-----	-----
BovGapC	c-gc--a-gg	-c---ccag-	-t---a-c--	-gct--t---	--c-----c-

FIG. 6C



	651				700
DysGapC	AAGCTATCGG	TCTTGTTATC	CCAGAATTGA	ATGGTAAACT	TGATGGTGCT
SpyGapC	-----	-----	-----c-t-	-c-----	-----
SeqGapC	-----	-----	-----g-	-c-----	-----
ParaUbGapC	---a-----	-----	--t---a-	-t-----	-----
UberGapc	---a-----	-----a-	-----a-	-t-----	-----
AgalGapCDNA	-----	a-----	-----g-	-c-----	---t-----
SiniGapC	---a-----	-----	-----a-	-t-----	-----
BovGapC	-g--cg-g--	caag--c--	--t--gc-c-	-c-g-g-g--	cact--catg
	701				750
DysGapC	GCACAACGTG	TTCCTGTTCC	AACTGGATCA	GTAAGTGAAGT	TGGTTGTAAC
SpyGapC	-----	-----	-----	-----g-	-----t---
SeqGapC	-----	-----	-----	-----g-	-----t---
ParaUbGapC	-----	-a-a-----	---a--t---	-----a---	-a-a---gt
UberGapc	-----	-----	-----	-----	-a-a---gt
AgalGapCDNA	-----	-----	-----	-----	-----
SiniGapC	-----	-----	-----	-----	-a-a---gt
BovGapC	--cttc--c-	-c--cac---	c-ac-tg--t	--tgtg--tc	--acctgccg
	751				800
DysGapC	TCTTGATAAA	AACGTTTCTG	TTGACGAAAT	CAACGCTGCT	ATGAAAGCTG
SpyGapC	-----c---	a--t-----	---c-----	-----t-t---	-----
SeqGapC	-----c---	a--t-----	---c-----	-----t---	-----
ParaUbGapC	---a-t---	--aac---a-	-a-----	t--t---ta	-----
UberGapc	-----	--aac---a-	-----	-----a	-----a-
AgalGapCDNA	-----	---taa---	-c-----g-	a-t-----	-----a-
SiniGapC	-----	--tac---a-	-a-----	---t-----	-----a-
BovGapC	c--g--g---	cct-ccaagt	a--t--g--	---gaag-tg	g----gcag-
	801				850
DysGapC	CTTCAAACGA	CAGTTTCGGT	TACACTGAAG	ATCCAATTGT	TTCTTCAGAT
SpyGapC	--t-----	-agc-t---	-----	-----	t-----
SeqGapC	--t-----	-agc-t---	-----	-----	t-----
ParaUbGapC	-ag-t--t-	-----at-	-----	-----	---a--t---
UberGapc	--g-----	-----a--a	-----	-c-----	-----t---
AgalGapCDNA	-ag-t-----	-----a---	--t-----	-----	---a--t---
SiniGapC	-ag-t-----	-----a---	-----	--g-t-----	---a-----
BovGapC	-gt--g-g-g	cc-tct-aag	gg--t-ct--	gctac-ct-a	ggaccag-t-
	851				900
DysGapC	ATCGTAGGCG	TGTCATA...	CGGTTCAATTG	TTTGACGCAA	CTCAAACATAA
SpyGapC	-----cg	-a-----	-----	-----c-a-	-----
SeqGapC	-----cg	-a-----	-----	-----c-a-	-----
ParaUbGapC	-----t-ta	---t-t...	-----a	--c-----	-----
UberGapc	---a-c--ta	--g-t---	-----	-----	-----
AgalGapCDNA	-----t-ta	-t-----	-----	-----	-----
SiniGapC	-----ta	-t-t---	-----a	-----	-----
BovGapC	g--tcct-cg	ac-tca-cag	--a-a-tcac	-c-tc-a-ct	tcg-tg--gg

FIG. 6D



	901				950
DysGapC	AGTTATGGAA	GTTGACGGAT	CACAATTGGT	TAAAGTTGTA	TCATGGTATG
SpyGapC	---aatggaa	-----c---t	ca-----	-----a	-----
SeqGapC	---tatggaa	-----t---t	ca-----	-----a	-----
ParaUbGapC	---a-----	-----t---	-t-----a-	-----	-----
UberGapc	---a-----	-----t---	-t-----a-	-----	-----
AgalGapCDNA	---t-----	-----c-t-	-c-----	-----	-----c-
SiniGapC	---a-----	-----t---	-t-----	-----	-----
BovGapC	g-ctggc-t-	-ccctcaacg	-c--c--t--	c--gc-ca--	--c-----c-

	951				1000
DysGapC	ACAATGAAAT	GTCTTACACT	GCTCAACTTG	TTCGTACACT	TGAGTATTTT
SpyGapC	----c-----	-----	-----	-a-----t--	-----c
SeqGapC	----c-----	-----	-----	-----	-----
ParaUbGapC	----t-----	-----	-----	a-----	-----
UberGapc	----c-----	-----	-a-----	-----t--	-----
AgalGapCDNA	-t--c-----	---a-----	t-a-----	-----	-----
SiniGapC	----t-----	-----	-----	-----t--	-----
BovGapC	----t--t-	tggc---gc	aaa--gg--	-----	-----

	1001		1018
DysGapC	GCAAAAATCG	CTAAATAA	
SpyGapC	-----t-	-----	
SeqGapC	-----	-----	
ParaUbGapC	-----	-----	
UberGapc	-----	-----	
AgalGapCDNA	-----	-----	
SiniGapC	-----	-----	
BovGapC	-----	-----	

FIG. 6E



	1				50
DysGapC	MVVKVGINGF	GRIGRLAFRR	IQNVEGVEVT	RIND.LTDPN	MLAHLKLYDT
SpyGapC	-----	-----	---I-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
PUberGapC	-----	-----	-----	-----	-----
UberGapC	-----	-----	-----	-----	-----
AgalGapC	-----	-----	-----	-----	-----
IniaeGapC	-----	-----	-----	-----	-----
BovGapC	-----	-----vt-a	af-sgk-div	a---pfi-lh	ymvymfq--s
	51				100
DysGapC	TQGRFDGTVE	VKEGGFEVNG	NFIKVSARD	PENIDWATDG	VEIVLEATGF
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
PUberGapC	-----	--d--d--	k-----k-	--q-----	-----
UberGapC	-----	--d-----	-----k-	-----	-----
AgalGapC	-----	-----	q-v-----e	-a-----	-----
IniaeGapC	-----	--d-----	s-v-----e	-a-----	-d-----
BovGapC	-h-k-n---k	aen-klvi--	ka-tifq---	-a--k-gda-	a-y-v-s--v
	101				150
DysGapC	FAKKEAAEKH	LHANGAKKVV	ITAPGGNDVK	TVVFNTNEDI	LDGTETVISG
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----p	-----	-----	qlfstltts-	-----
PUberGapC	---a-----	--e-----	-----d--	-----	-----
UberGapC	---a-----	-----	-----d--	-----	-----
AgalGapC	--s--k-gq-	i-e-----	-----	-----	-----
IniaeGapC	--s-a---q-	i-----	-----	---y-----	-----
BovGapC	-ttm-k-ga-	-.kg---r-i	-s--sa.-ap	mf-mgv--ek	ynn-lkiv-n

FIG. 7A





	151				200
DysGapC	ASCTTNCLAP	MAKALHDAFG	IQKGLMTTIIH	AYTGDQMILD	GPHRGGDLRR
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----v-	-hrg-----
PUberGapC	-----	----q-n--	v-----	-----	-----
UberGapC	-----	----q-n--	v-----	-----	-----
AgalGapC	-----	----q-n--	v-----	-----	-----
IniaeGapC	-----	----q-n--	v-----	g-----v-	-----
BovGapC	-----	1--vih-h--	ive-----v-	-i-at-ktv-	--.s-klw-d
	201				250
DysGapC	ARAGAANIVP	NSTGAAKAIG	LVIPELNGKL	DGAAQRPVVP	TGSVTELVVT
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----r-----	-----	-----	-----
PUberGapC	-----n-----	-----	-----	-----	-----av
UberGapC	-----s-----	-----	-----	-----	-----av
AgalGapC	-----	-----	-----	-----	-----a-
IniaeGapC	---a-----	-----	-----	-----	-----av
BovGapC	g-ga-q--i-	a-----v-	k-----	t-m-f---t-	nv--vd-tcr
	251				300
DysGapC	LDKNVSVDEI	NAAMKAASND	S....FGYTE	DPIVSSDIVG	VSYGSLFDAT
SpyGapC	-----	-s-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
PUberGapC	-n-et--e--	-sv---a--	....y---	-----	m-f-----
UberGapC	-e-et--e--	-----a--	....y---	-----i-	ma-----
AgalGapC	-e-d-t-e-v	-----a--	....y---	-----	i-----
IniaeGapC	-e-dt--e--	-----a--	....y---	-a-----	i-----
BovGapC	-e-paky---	kkvv-q--eg	plkgilg---	-qv--c-fns	dths-t---g
	301				341
DysGapC	QTKVMEVDGS	QLVKVVSWD	NEMSYTAQLV	RTLEYFAKIA	K
SpyGapC	-----	-----	-----	-----	-
SeqGapC	-----	-----	-----	-----	-
PUberGapC	----qt---n	-----	-----d	-----	-
UberGapC	----qt---n	-----	-----	-----	-
AgalGapC	----qt---n	-----	-----s---	-----	-
IniaeGapC	----qt---n	-----	-----	-----	-
BovGapC	agial...nd	hf--li----	--fg-sk---	-----	~

FIG. 7B

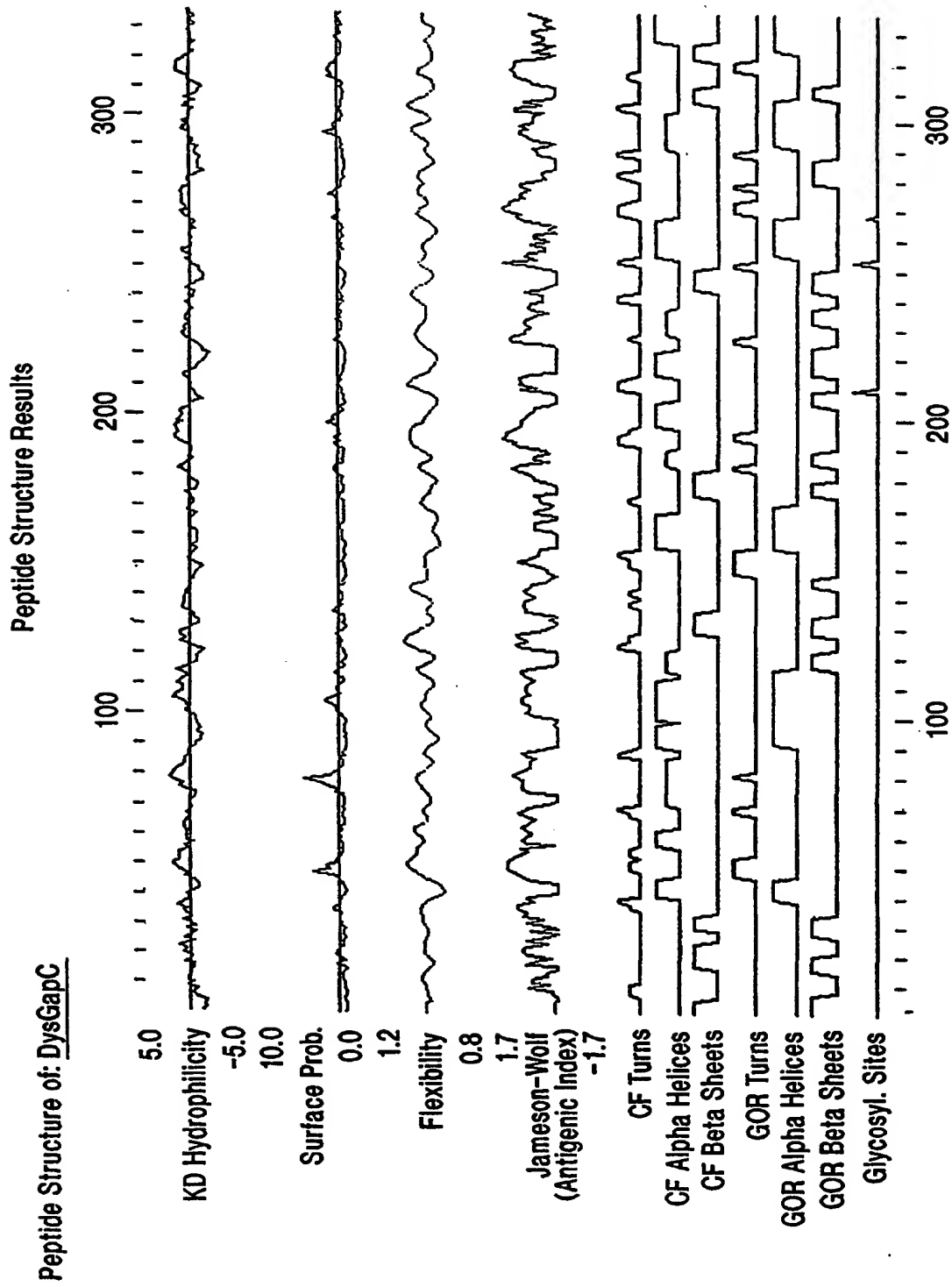


FIG. 8



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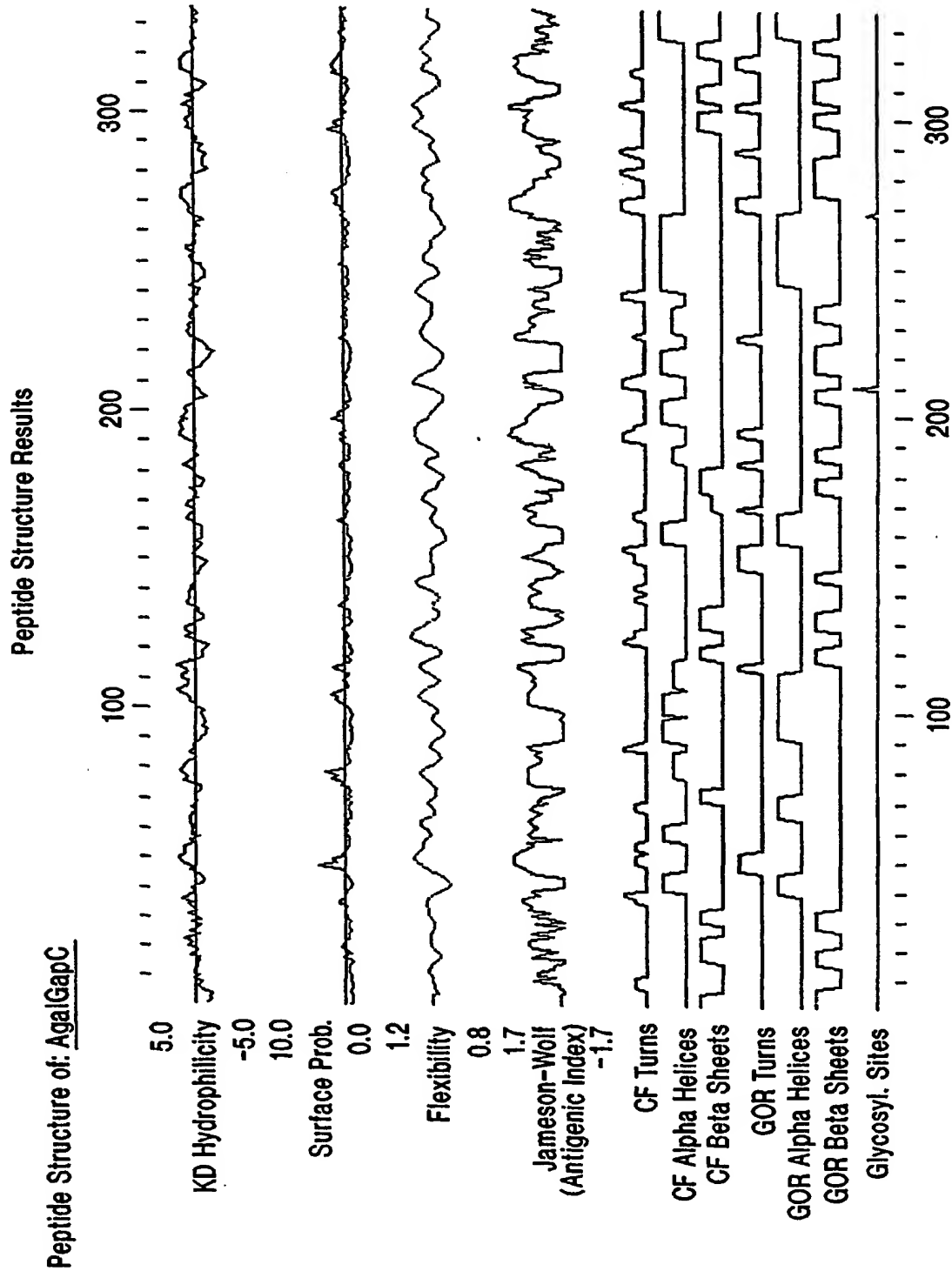


FIG. 9



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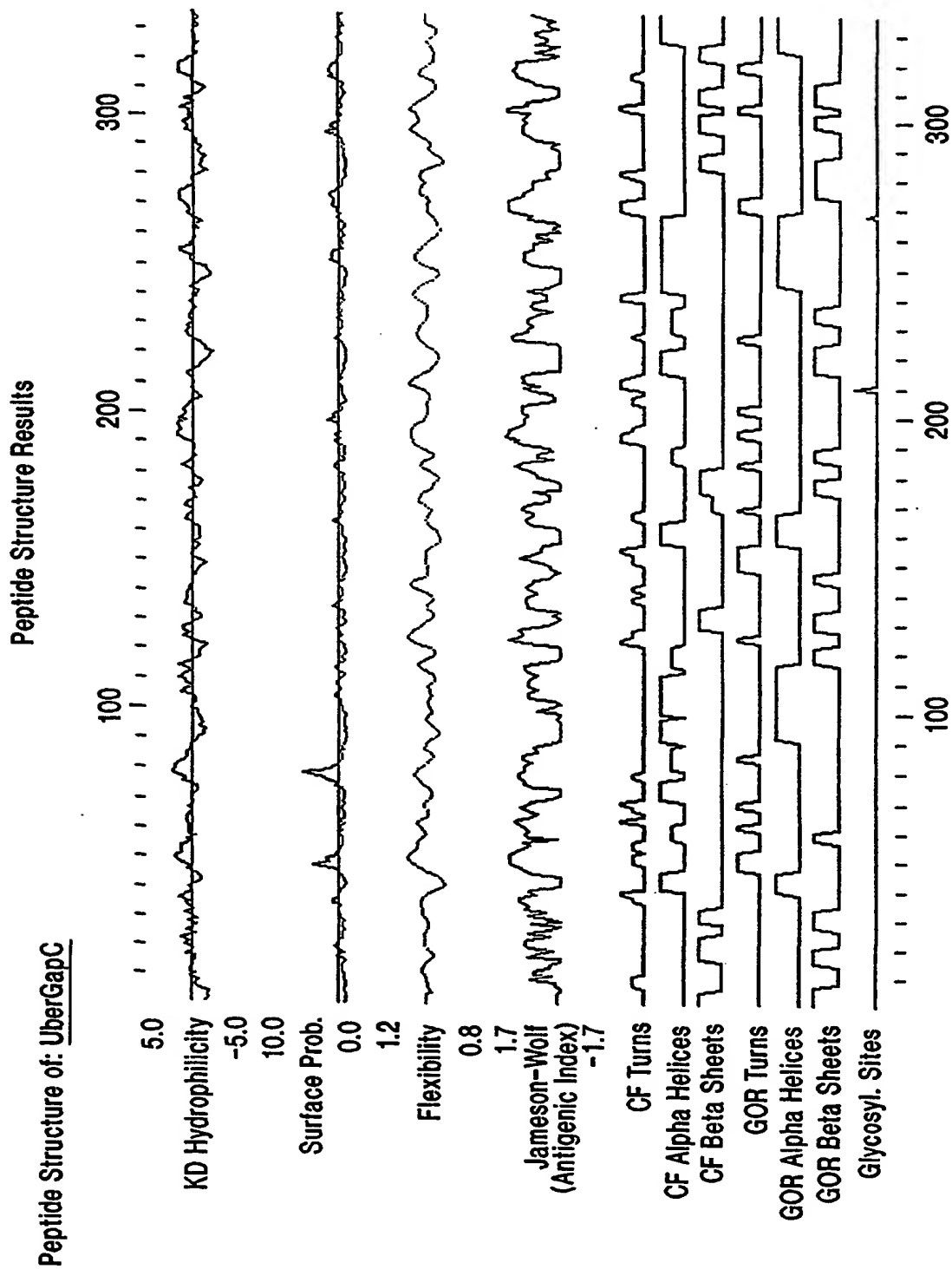


FIG. 10



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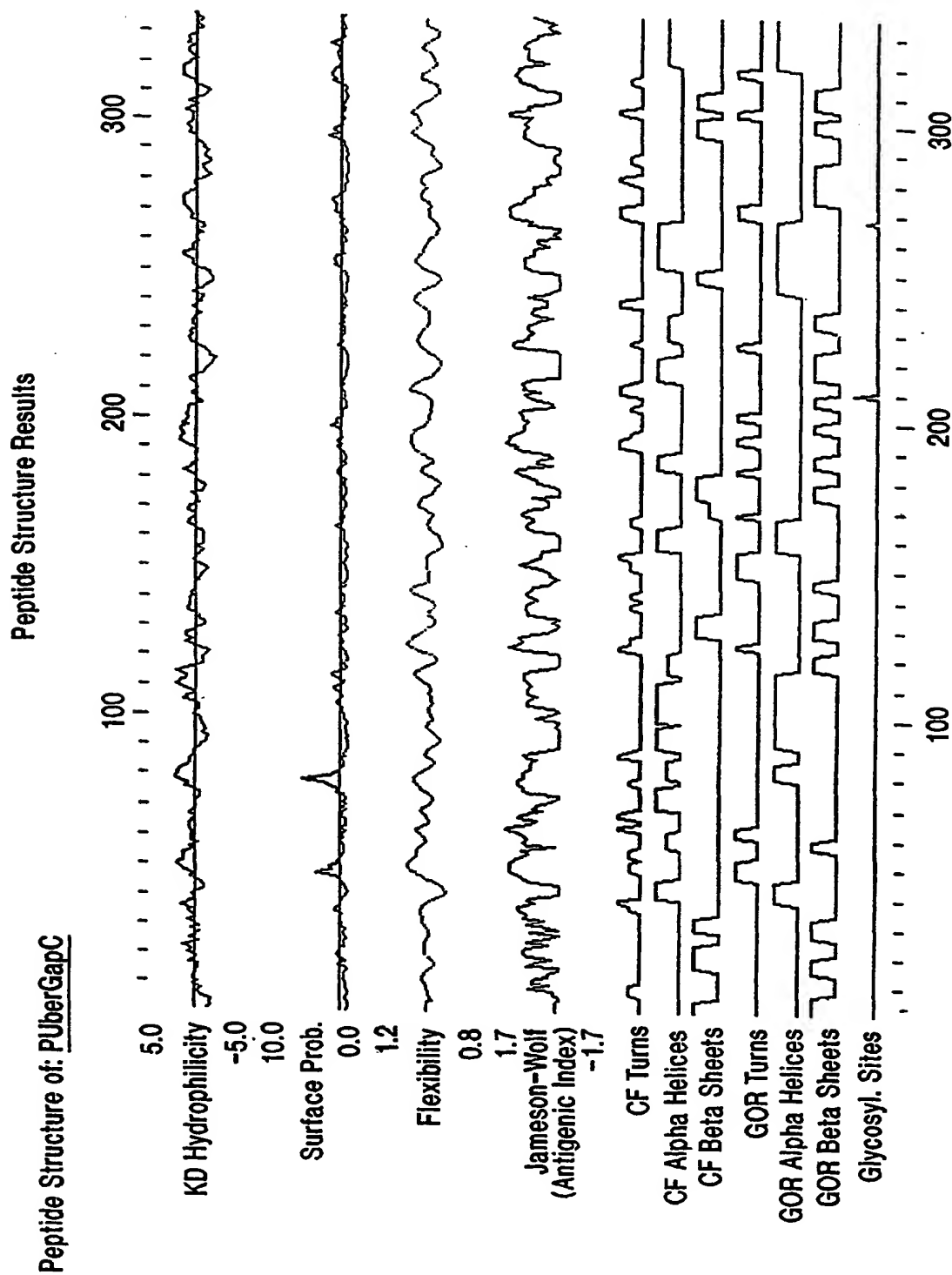


FIG. 11



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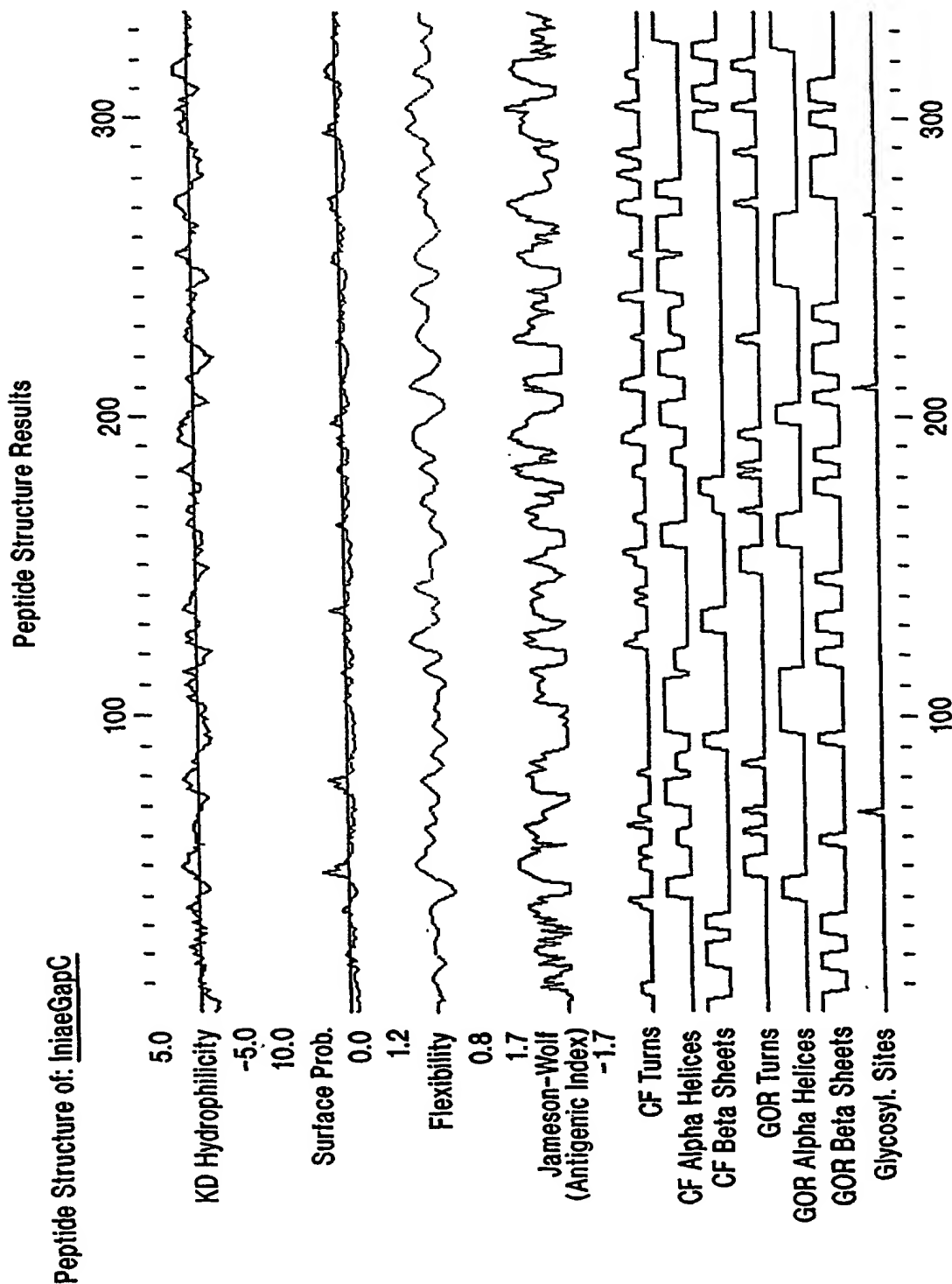


FIG. 12



Peptide Structure Results

○ KD Hydrophilicity  $\geq 1.3$   
◇ KD Hydrophobicity  $\geq 1.3$

Peptide Structure of: DysGapC

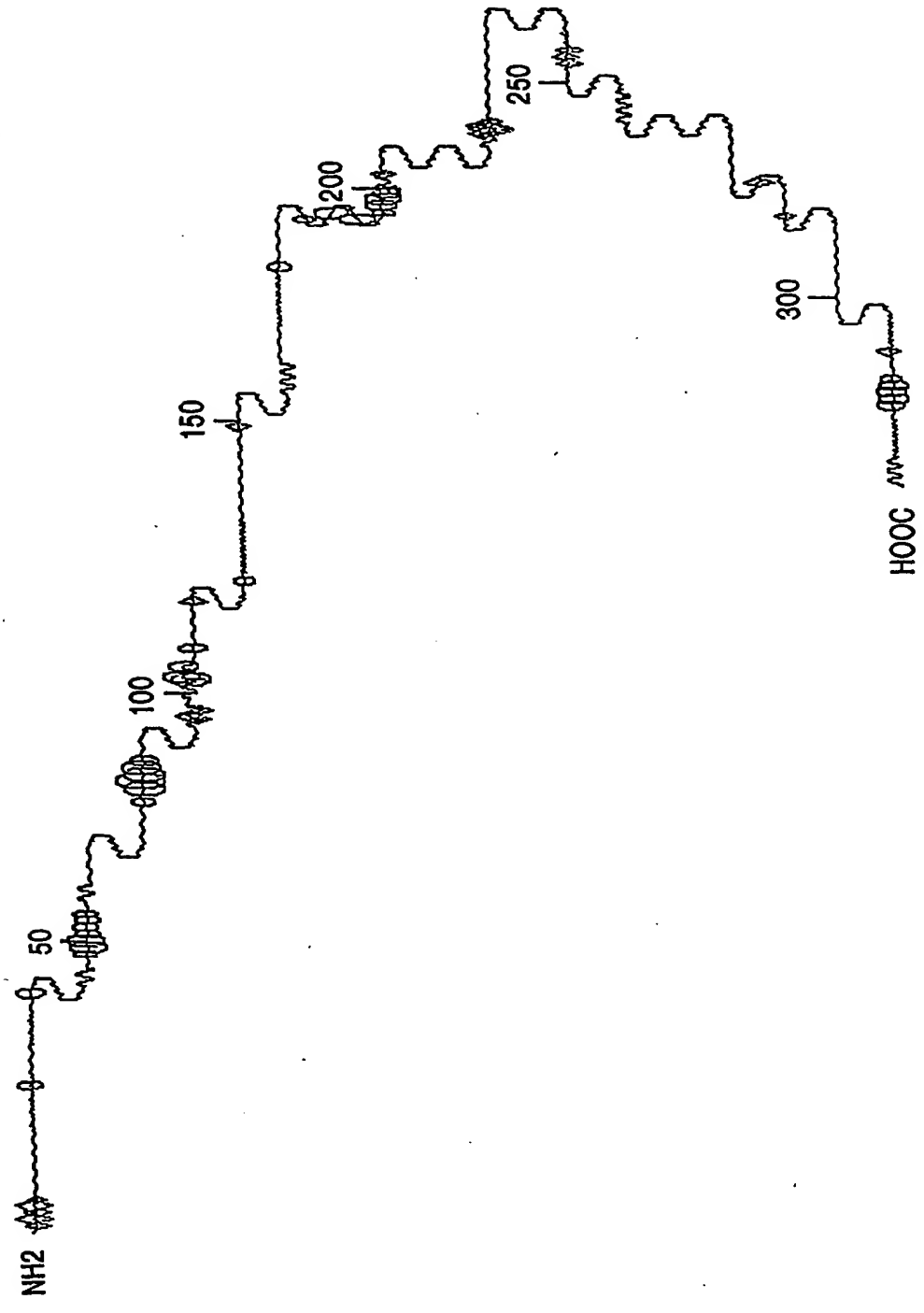


FIG. 13



Peptide Structure Results

Peptide Structure of: AgalGapC

○ KD Hydrophilicity  $\geq 1.3$   
◇ KD Hydrophobicity  $\geq 1.3$

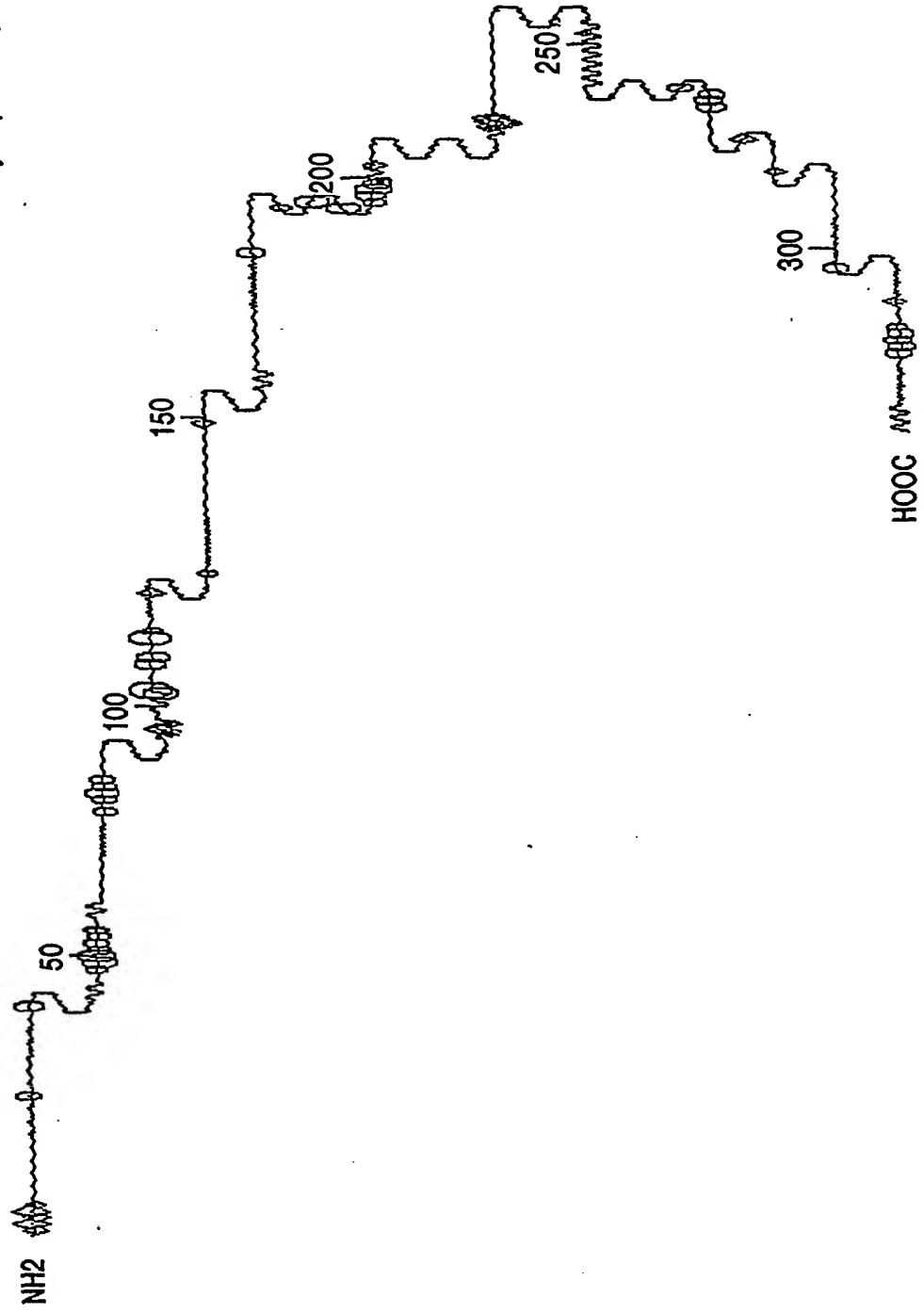


FIG. 14





Peptide Structure Results

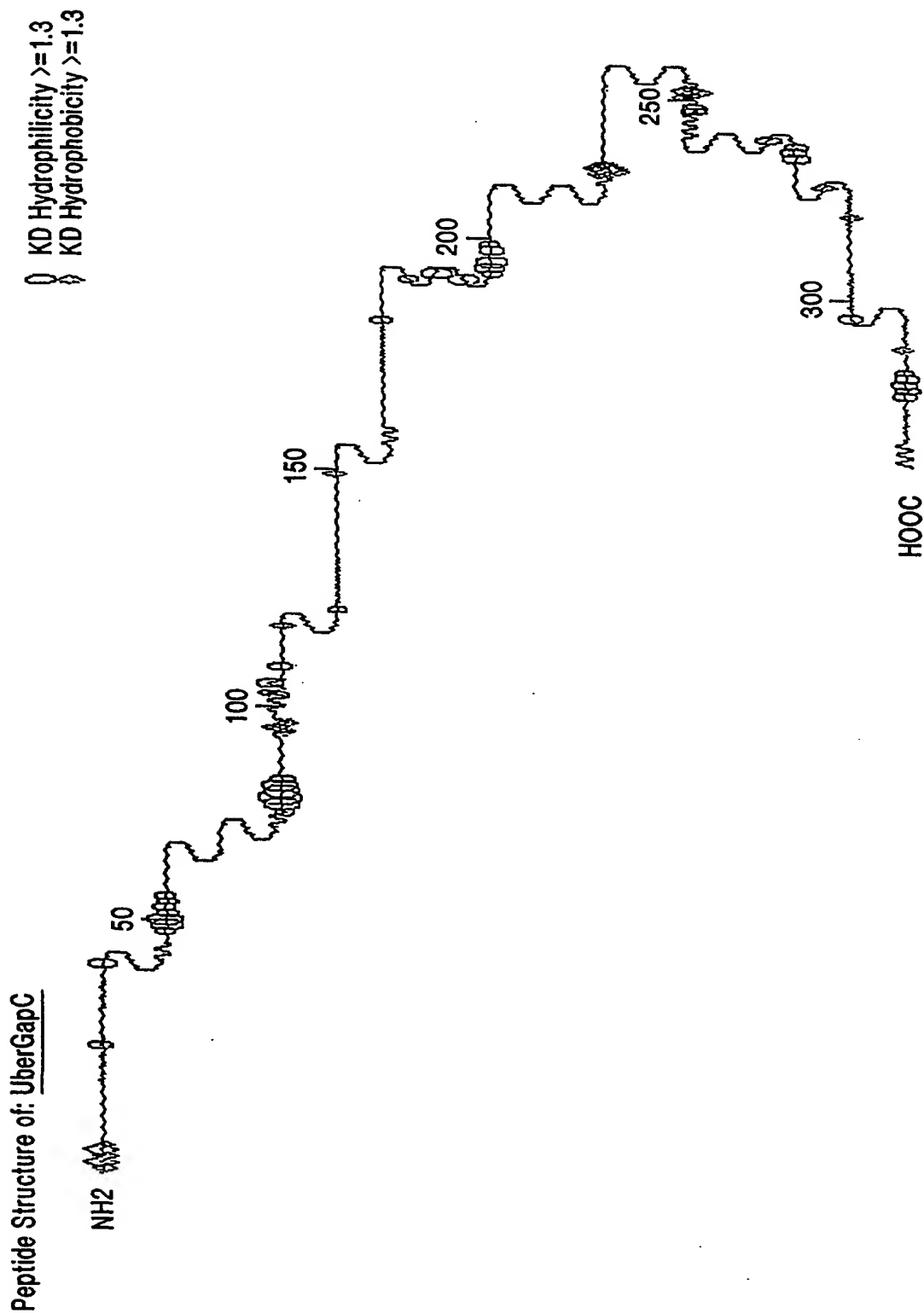


FIG. 15



# Peptide Structure Results

Peptide Structure of: PUberGapC

○ KD Hydrophilicity  $\geq 1.3$   
 ◇ KD Hydrophobicity  $\geq 1.3$

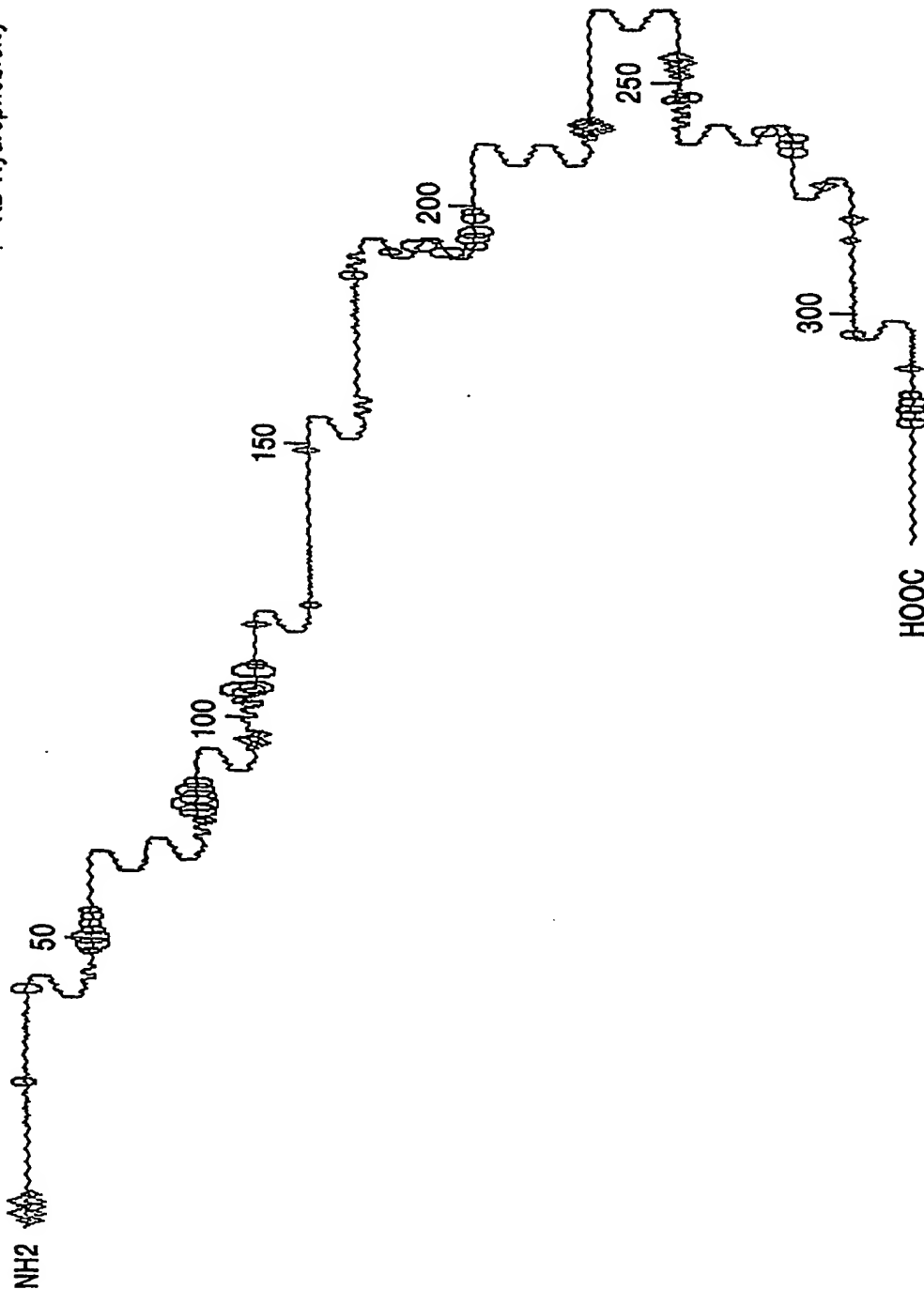


FIG. 16



Peptide Structure Results

Peptide Structure of: IniaeGapC

○ KD Hydrophilicity  $\geq 1.3$   
◇ KD Hydrophobicity  $\geq 1.3$

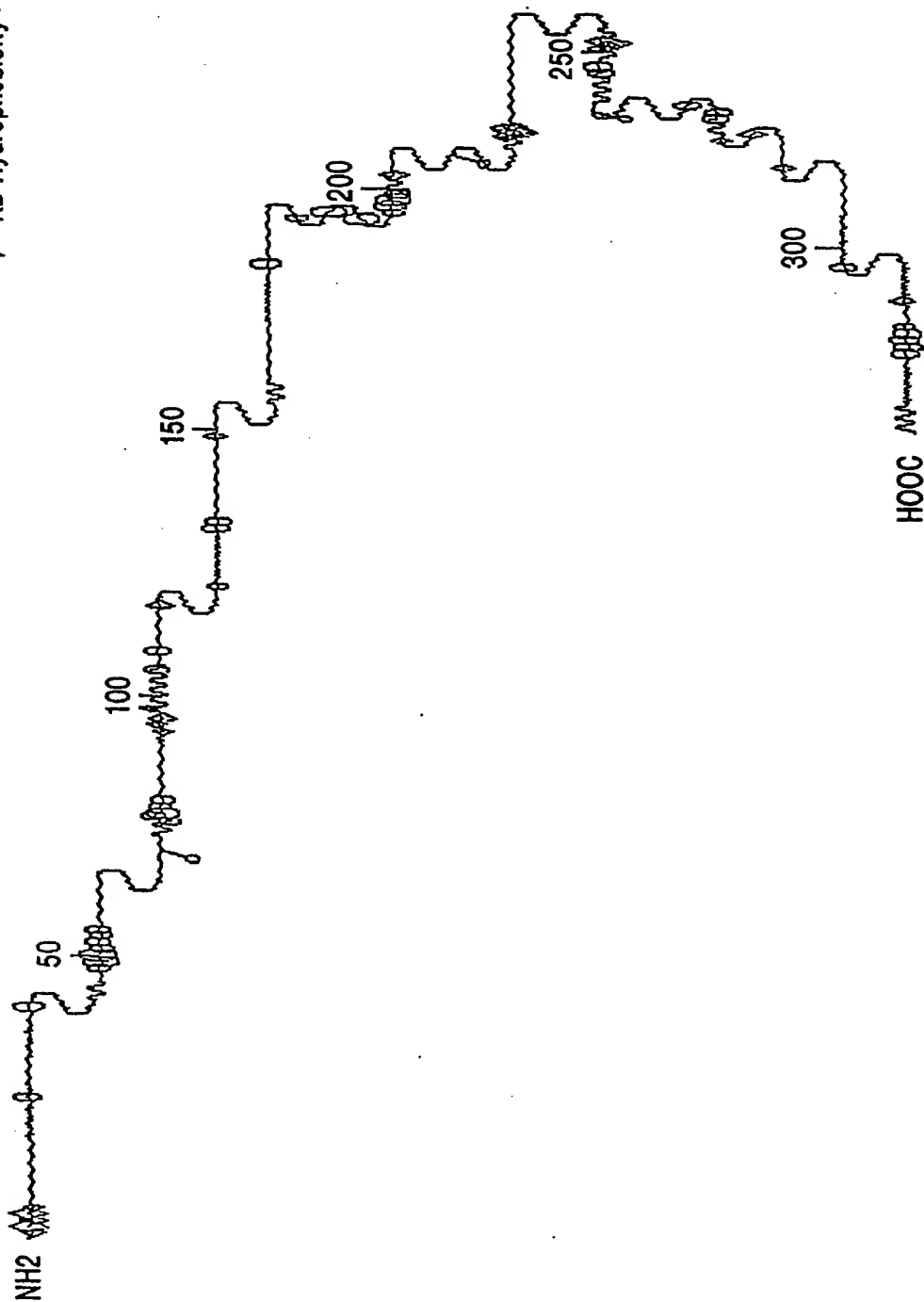


FIG. 17

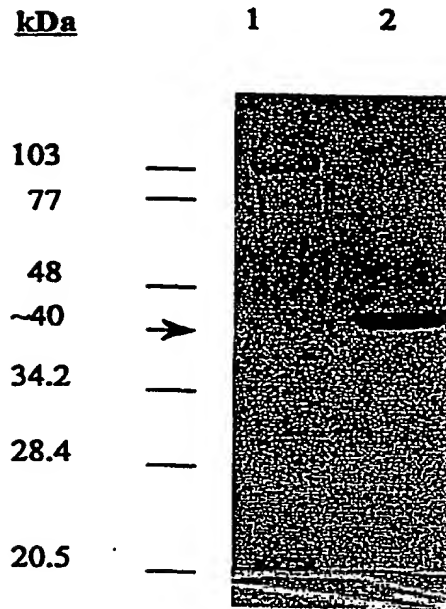


FIG. 18

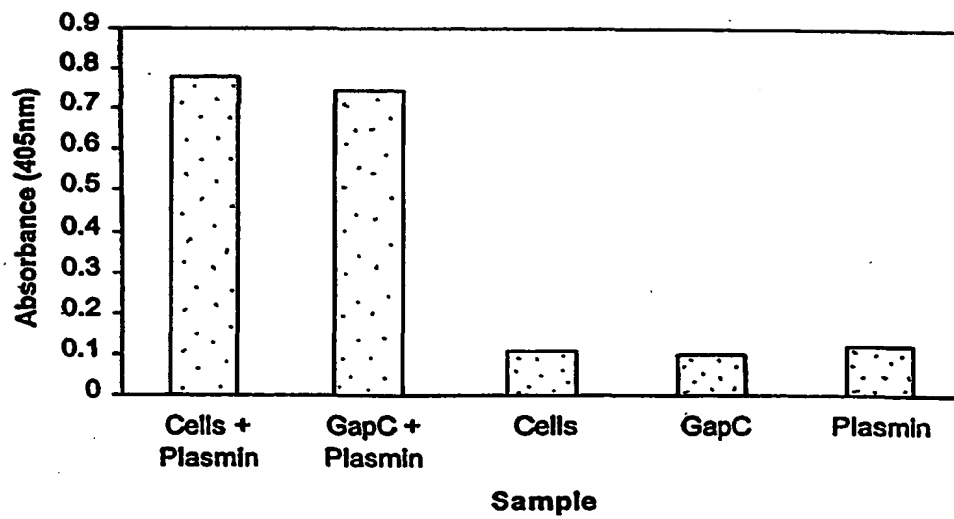


FIG. 19



Percentage of quaters infected with *S. dysgalactiae* per group

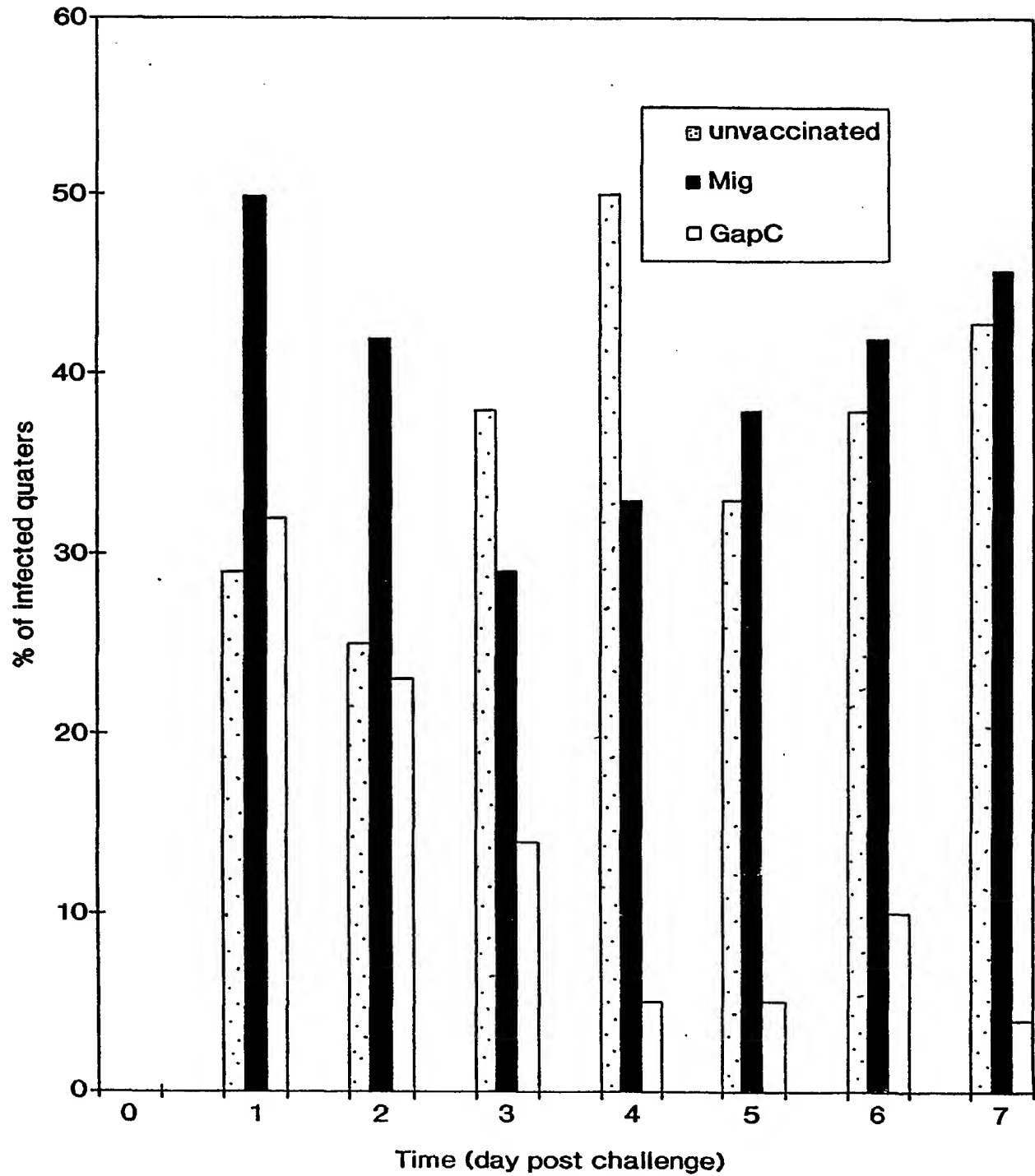


FIG. 20



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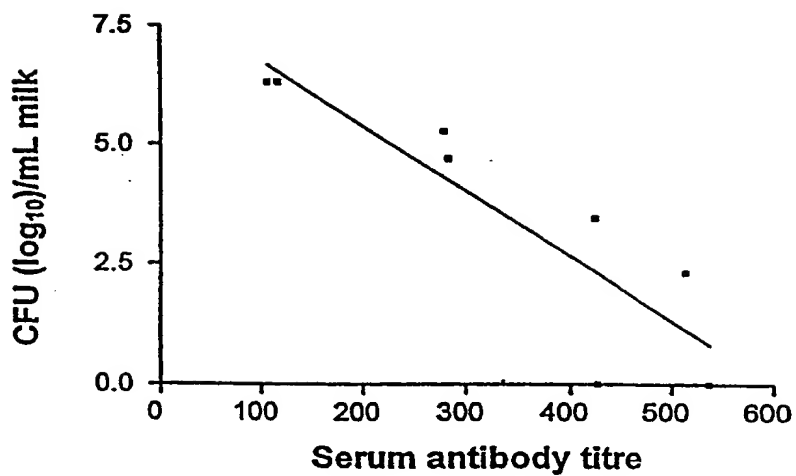


FIG. 21

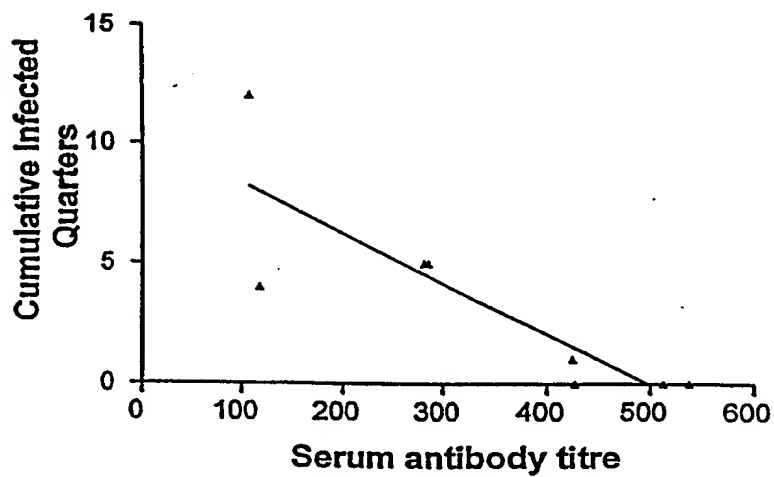


FIG. 22

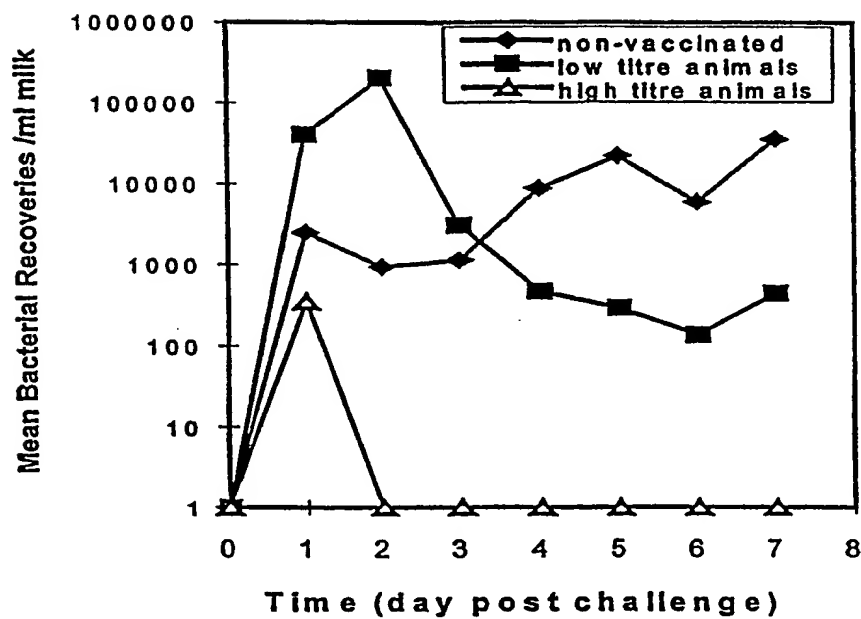


FIG. 23

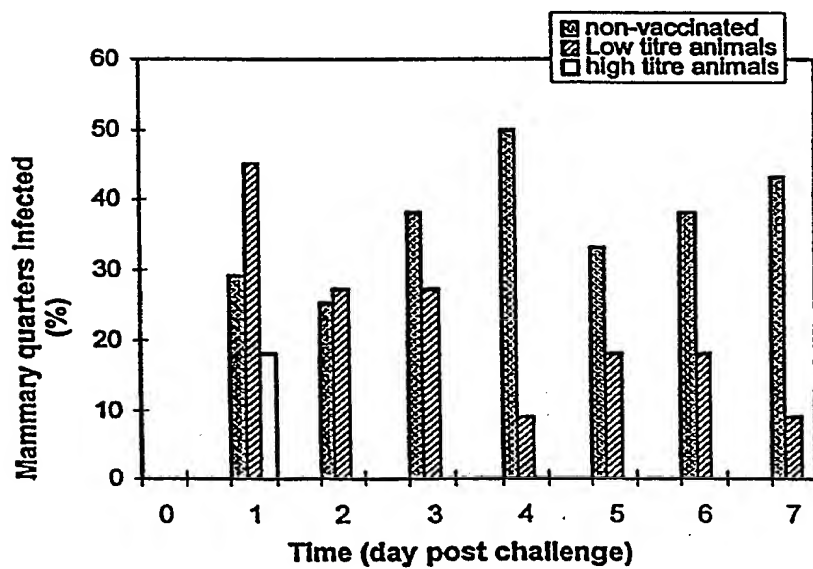


FIG. 24



Mean Somatic Cell Counts (SCC) per group

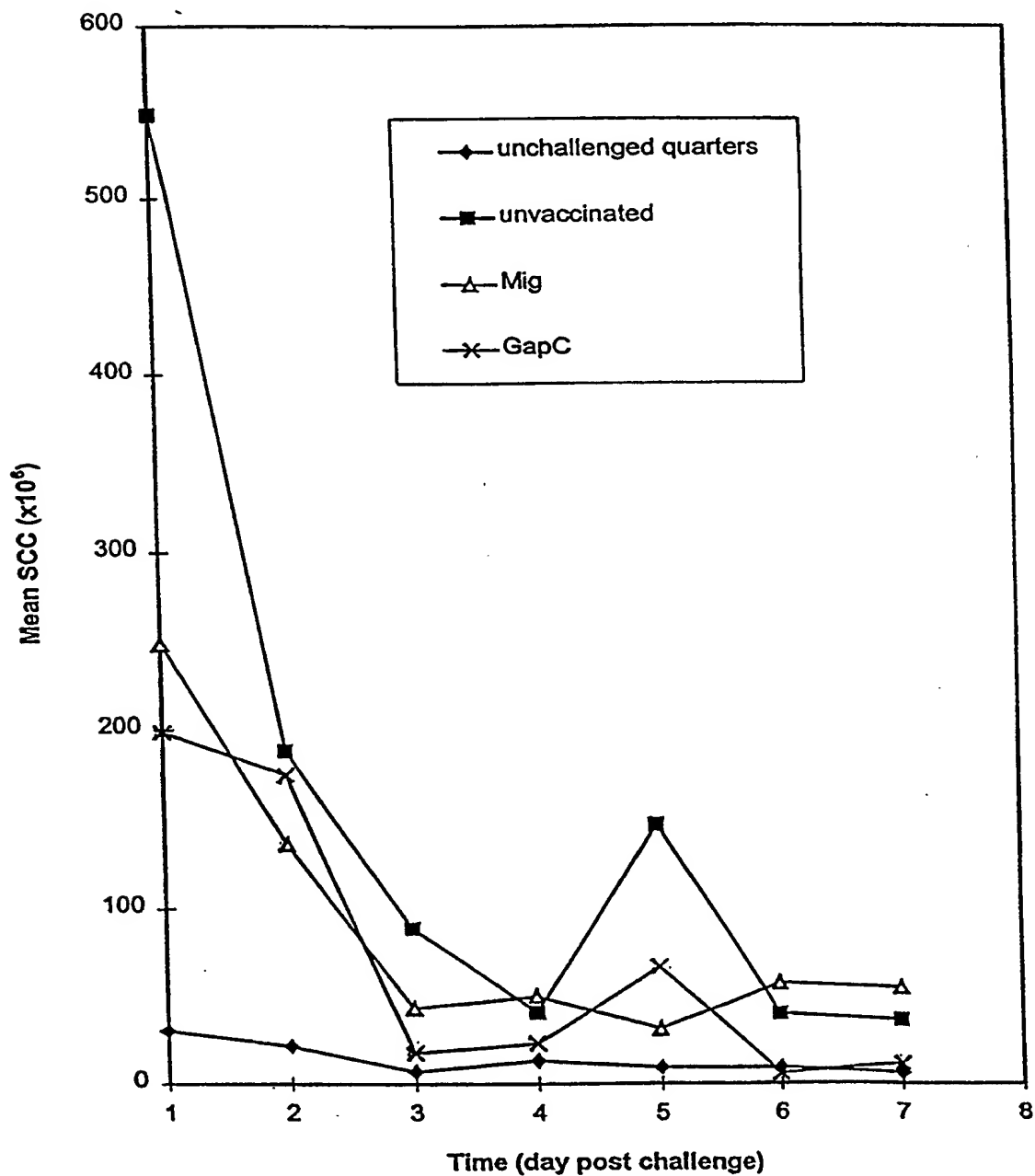
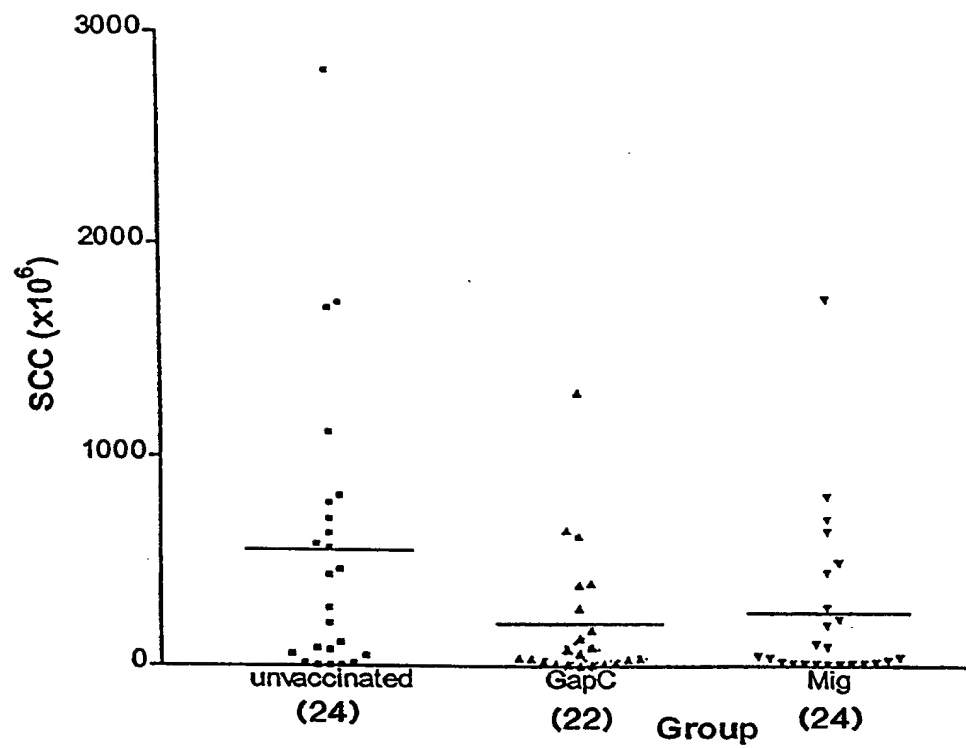


FIG. 25





**Somatic Cell Counts (SCC):  
One day post challenge**



**FIG. 26**

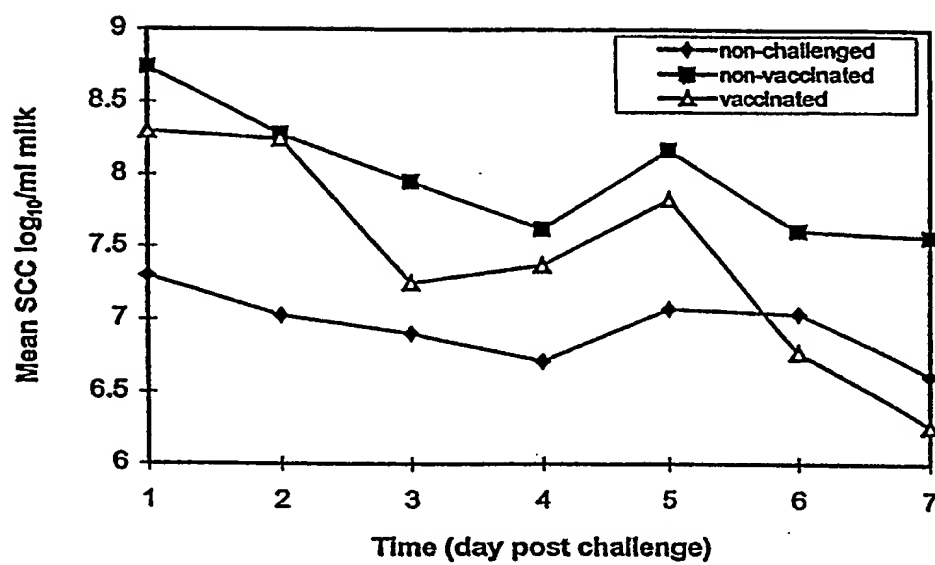


FIG. 27